

Table III

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) + 12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) + 12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) + 12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) + 12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) + 12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) + 12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) + 12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) + 12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (1 of 2)

[illegible]

Table IV (2 of 2)

[illegible]

[illegible]

[illegible]

GENE DESCRIPTION	HGNC ID	SNP ID	CONTIG_NUM	CONTIG_POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO.)	FLANK_SEQ REF (SEQ ID NO.)	FLANK_SEQ ALT (SEQ ID NO.)	REFSEQ_FLANK REF (SEQ ID NO.)
Ambopodipase P (membrane-bound)	XPINPE2	AE10041	1	127	P	P	Exon2	Start	0	CCC	CCG	AAB9534.1	607	4	37	100	163
Bradykinin Receptor B1	BDKRB1	AE10341	6	307	R	Q	Exon2	Missense	0	CCG	CAG	NP_000701.1	317	6	60	123	186
Bradykinin Receptor B1	BDKRB1	AE10342	4	273	P	P	Exon2	Start	0	CCG	CCA	NP_000701.1	41	10	61	124	187
Tachykinin Receptor 1	TACR1	AE10641	1	614	F	F	Exon1	Start	1	TTT	TTC	NP_001048.1	111	16	81	144	207
Tachykinin Receptor 1	TACR1	AE10642	2	769	I	I	Exon2	Start	1	ATC	ATA	NP_001048.1	154	18	82	145	208
Tachykinin Receptor 1	TACR1	AE10647	6	611	S	S	Exon5	Start	1	TGG	TCA	NP_001048.1	378	20	87	150	213
C1 Esterase Inhibitor	C1NH	AE10543	5	366	S	S	Exon7	Start	0	AGC	AGT	NP_000053.1	406	24	90	153	216
C1 Esterase Inhibitor	C1NH	AE10544	7	588	V	A	Exon3	Missense	0	GTT	GCT	NP_000053.1	56	26	91	154	217
C1 Esterase Inhibitor	C1NH	AE10555	7	897	A	G	Exon3	Missense	0	GCA	GGA	NP_000053.1	159	28	92	155	218
C1 Esterase Inhibitor	C1NH	AE10546	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000053.1	480	30	93	156	219
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE10741	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	186	34	94	157	220
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE10743	2	695	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159	222
Bradykinin Receptor B1	BDKRB1	AE10346	1	67	N	N	Exon3	Start	0	AAC	AAT	NP_000701.1	114	556	579	611	643
Bradykinin Receptor B1	BDKRB1	AE10347	1	181	R	R	Exon3	Start	0	AGG	AGA	NP_000701.1	152	558	580	612	644
Bradykinin Receptor B1	BDKRB1	AE10348	1	296	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	560	581	613	645
Bradykinin Receptor B1	BDKRB1	AE10349	2	136	E	E	Exon3	Start	0	GAG	GAA	NP_000701.1	233	562	582	614	646
Bradykinin Receptor B2	BDKRB2	AE104419	7	339	R	C	Exon2	Missense	1	CGT	TGT	NP_000814.1	14	564	584	616	648
Bradykinin Receptor B2	BDKRB2	AE104424	4	918	D	D	Exon3	Start	1	GAT	GAC	NP_000814.1	311	568	589	621	653
Bradykinin Receptor B2	BDKRB2	AE104425	4	1048	G	E	Exon3	Missense	1	GCG	GAG	NP_000814.1	354	568	590	622	654
Angiotensin Converting Enzyme 2	ACE2	AE10947	15	241	N	N	Exon16	Start	1	AAT	AAC	AA176220.1	690	843	891	833	665
Protease Inhibitor 4	P4	AE11042	2	526	F	F	Exon2	Start	0	TTC	TTT	NP_000208.1	233	574	603	635	667
Protease Inhibitor 4	P4	AE11045	4	563	S	S	Exon1	Start	0	AGT	AGC	NP_000208.1	199	576	606	638	670

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37

Table VII B

DNA panel	Coriell Catalog #	Sample Description	XPNEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50/AA panel	14537	African American								
HD 50/AA panel	14583	African American								
HD 50/AA panel	14681	African American								
HD 50/AA panel	14687	African American								
HD 50/AA panel	14697	African American								
HD 50/AA panel	14699	African American								
HD 50/AA panel	14720	African American								
HD 50/AA panel	14746	African American								
HD 50/AA panel	14754	African American								
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HD 50/AA panel	14771	African American								
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HD 50/AA panel	14783	African American								
HD 50/AA panel	14826	African American								
HD 50/AA panel	14837	African American								
HD 50/AA panel	14862	African American								
HD 50/AA panel	14863	African American								
HD 50/AA panel	14864	African American								
HD 50/AA panel	14892	African American								
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HD 50/AA panel	14924	African American								
HD 50/AA panel	14925	African American								
HD 50/AA panel	14932	African American								
HD 50/AA panel	14933	African American								
HD 100/CAU panel	NA 17201	Caucasian								
HD 100/CAU panel	17202	Caucasian								
HD 100/CAU panel	17203	Caucasian								
HD 100/CAU panel	17204	Caucasian								
HD 100/CAU panel	17205	Caucasian								
HD 100/CAU panel	17206	Caucasian								
HD 100/CAU panel	17207	Caucasian								
HD 100/CAU panel	17208	Caucasian								
HD 100/CAU panel	17209	Caucasian								
HD 100/CAU panel	17210	Caucasian								

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Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPBPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian								
HD 100 CAU panel	17212	Caucasian								
HD 100 CAU panel	17213	Caucasian								
HD 100 CAU panel	17214	Caucasian								
HD 100 CAU panel	17215	Caucasian								
HD 100 CAU panel	17216	Caucasian								
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HD 100 CAU panel	17251	Caucasian								
HD 100 CAU panel	17252	Caucasian								
HD 100 CAU panel	17253	Caucasian								
HD 100 CAU panel	17254	Caucasian								

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer	PCR Left primer (SEQ ID NO.)	PCR Right primer	PCR Right primer (SEQ ID NO.)
Antropodipase P (membrane-bound)	XPNIPE2	AE10051	Exon20	0	AE10051p7b	XPNIPE2_X20a	AGTGTCTCTCTCTCTCTCTCT	287	TATTCACACTGAGGCTTGGG	360
Antropodipase P (membrane-bound)	XPNIPE2	AE10052	Intron3	0	AE10052p10	XPNIPE2_X3a	CAGCCGACGACATCTTAATCTA	288	TCTCTACTTCCCTGCTTGG	361
Antropodipase P (membrane-bound)	XPNIPE2	AE10053	Intron15	0	AE10053p8	XPNIPE2_X15a	TAGCTGTCTCTCTCTCTCTCT	289	ATAGGATGAGGCTCAGCTTGG	362
Antropodipase P (membrane-bound)	XPNIPE2	AE10054	Intron15	0	AE10054p2	XPNIPE2_X15a	TAGCTGTCTCTCTCTCTCTCT	300	ATAGGATGAGGCTCAGCTTGG	363
Antropodipase P (membrane-bound)	XPNIPE2	AE10055	Intron1	0	AE10055p28	XPNIPE2_X1a	TGATGAGACGAGCTTGGTG	301	ACAGAAAAGAGACTCGGGC	364
Antropodipase P (membrane-bound)	XPNIPE2	AE10056	Intron7	0	AE10056p28	XPNIPE2_X7a	CGAGGCTGGGATACATG	302	GGCCTGAAATCTGCAATT	365
Antropodipase P (membrane-bound)	XPNIPE2	AE10057	Intron7	0	AE10057p28	XPNIPE2_X7a	CGAGGCTGGGATACATG	303	GGCCTGAAATCTGCAATT	366
Antropodipase P (membrane-bound)	XPNIPE2	AE10058	Intron10	0	AE10058p38	XPNIPE2_X10a	CTCTCTTGGACCTCGAGAAC	304	CGTGTCTCTCTCTCTCTCT	367
Antropodipase P (membrane-bound)	XPNIPE2	AE10059	Intron10	0	AE10059p38	XPNIPE2_X10a	CTCTCTTGGACCTCGAGAAC	305	CGTGTCTCTCTCTCTCTCT	368
Antropodipase P (membrane-bound)	XPNIPE2	AE10060	Intron7	0	AE10060p28	XPNIPE2_X7a	CGAGGCTGGGATACATG	306	GGCCTGAAATCTGCAATT	369
Antropodipase P (membrane-bound)	XPNIPE2	AE10061	Intron13	0	AE10061p50	XPNIPE2_X13a	TAATGACAGCTCAGGGCTTG	307	CAGGCTCAGGCTCTTCAAT	370
Antropodipase P (membrane-bound)	XPNIPE2	AE10062	Intron13	0	AE10062p50	XPNIPE2_X13a	TAATGACAGCTCAGGGCTTG	308	CAGGCTCAGGCTCTTCAAT	371
Antropodipase P (membrane-bound)	XPNIPE2	AE10063	Intron13	0	AE10063p50	XPNIPE2_X13a	TAATGACAGCTCAGGGCTTG	309	CAGGCTCAGGCTCTTCAAT	372
Antropodipase P (membrane-bound)	XPNIPE2	AE10064	Exon1	0	AE10064p2	XPNIPE2_X1a	TGATGAGACGAGCTTGGTG	310	ACAGAAAAGAGACTCGGGC	373
Antropodipase P (membrane-bound)	XPNIPE2	AE10065	Exon1	0	AE10065p28	XPNIPE2_X1a	TGATGAGACGAGCTTGGTG	311	ACAGAAAAGAGACTCGGGC	374
Antropodipase P (membrane-bound)	XPNIPE2	AE10066	Intron8	0	AE10066p58	XPNIPE2_X8a	GGCCATCTCTTAATGAGTAC	312	TCAGGCTACCTTGTCTCT	375
Antropodipase P (membrane-bound)	XPNIPE2	AE10067	Intron17	0	AE10067p58	XPNIPE2_X17a	CCCTCTCTTAGGACACATC	313	CTGCTGGCATCTCTCACTAC	376
Antropodipase P (membrane-bound)	XPNIPE2	AE10068	Intron17	0	AE10068p58	XPNIPE2_X17a	CCCTCTCTTAGGACACATC	314	CTGCTGGCATCTCTCACTAC	377
Antropodipase P (membrane-bound)	XPNIPE2	AE10069	Intron15	0	AE10069p58	XPNIPE2_X15a	TAGCTGTCTCTCTCTCTCT	315	ATAGGATGAGGCTCAGCTTGG	378
Antropodipase P (membrane-bound)	XPNIPE2	AE10070	Intron21	0	AE10070p82	XPNIPE2_X21f1a	GGACTATGGTGAAGCTGGAG	316	CAAGAAGCCCTGTCTCTG	379
Antropodipase P (membrane-bound)	XPNIPE2	AE10071	Exon21	0	AE10071p82	XPNIPE2_X21f1a	GGACTATGGTGAAGCTGGAG	317	CAAGAAGCCCTGTCTCTG	380
Antropodipase P (membrane-bound)	XPNIPE2	AE10072	Exon21	0	AE10072p82	XPNIPE2_X21f1a	GGACTATGGTGAAGCTGGAG	318	CAAGAAGCCCTGTCTCTG	381
Antropodipase P (membrane-bound)	XPNIPE2	AE10073	Exon21	0	AE10073p82	XPNIPE2_X21f1a	GGACTATGGTGAAGCTGGAG	319	CAAGAAGCCCTGTCTCTG	382
Antropodipase P (membrane-bound)	XPNIPE2	AE10074	Exon2	0	AE10074p34	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	320	ATGAAAGCCAGCTCTTGGT	383
Antropodipase P (membrane-bound)	XPNIPE2	AE10075	Exon3	0	AE10075p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	321	ATGAAAGCCAGCTCTTGGT	384
Antropodipase P (membrane-bound)	XPNIPE2	AE10076	Exon3	0	AE10076p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	322	ATGAAAGCCAGCTCTTGGT	385
Antropodipase P (membrane-bound)	XPNIPE2	AE10077	Exon3	0	AE10077p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	323	ATGAAAGCCAGCTCTTGGT	386
Antropodipase P (membrane-bound)	XPNIPE2	AE10078	Exon3	0	AE10078p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	324	ATGAAAGCCAGCTCTTGGT	387
Antropodipase P (membrane-bound)	XPNIPE2	AE10079	Exon3	0	AE10079p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	325	ATGAAAGCCAGCTCTTGGT	388
Antropodipase P (membrane-bound)	XPNIPE2	AE10080	Exon3	0	AE10080p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	326	ATGAAAGCCAGCTCTTGGT	389
Antropodipase P (membrane-bound)	XPNIPE2	AE10081	Exon3	0	AE10081p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	327	ATGAAAGCCAGCTCTTGGT	390
Antropodipase P (membrane-bound)	XPNIPE2	AE10082	Exon3	0	AE10082p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	328	ATGAAAGCCAGCTCTTGGT	391
Antropodipase P (membrane-bound)	XPNIPE2	AE10083	Exon3	0	AE10083p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	329	ATGAAAGCCAGCTCTTGGT	392
Antropodipase P (membrane-bound)	XPNIPE2	AE10084	Exon3	0	AE10084p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	330	ATGAAAGCCAGCTCTTGGT	393
Antropodipase P (membrane-bound)	XPNIPE2	AE10085	Exon3	0	AE10085p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	331	ATGAAAGCCAGCTCTTGGT	394
Antropodipase P (membrane-bound)	XPNIPE2	AE10086	Exon3	0	AE10086p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	332	ATGAAAGCCAGCTCTTGGT	395
Antropodipase P (membrane-bound)	XPNIPE2	AE10087	Exon3	0	AE10087p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	333	ATGAAAGCCAGCTCTTGGT	396
Antropodipase P (membrane-bound)	XPNIPE2	AE10088	Exon3	0	AE10088p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	334	ATGAAAGCCAGCTCTTGGT	397
Antropodipase P (membrane-bound)	XPNIPE2	AE10089	Exon3	0	AE10089p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	335	ATGAAAGCCAGCTCTTGGT	398
Antropodipase P (membrane-bound)	XPNIPE2	AE10090	Exon3	0	AE10090p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	336	ATGAAAGCCAGCTCTTGGT	399
Antropodipase P (membrane-bound)	XPNIPE2	AE10091	Exon3	0	AE10091p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	337	ATGAAAGCCAGCTCTTGGT	400
Antropodipase P (membrane-bound)	XPNIPE2	AE10092	Exon3	0	AE10092p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	338	ATGAAAGCCAGCTCTTGGT	401
Antropodipase P (membrane-bound)	XPNIPE2	AE10093	Exon3	0	AE10093p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	339	ATGAAAGCCAGCTCTTGGT	402
Antropodipase P (membrane-bound)	XPNIPE2	AE10094	Exon3	0	AE10094p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	340	ATGAAAGCCAGCTCTTGGT	403
Antropodipase P (membrane-bound)	XPNIPE2	AE10095	Exon3	0	AE10095p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	341	ATGAAAGCCAGCTCTTGGT	404
Antropodipase P (membrane-bound)	XPNIPE2	AE10096	Exon3	0	AE10096p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	342	ATGAAAGCCAGCTCTTGGT	405
Antropodipase P (membrane-bound)	XPNIPE2	AE10097	Exon3	0	AE10097p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	343	ATGAAAGCCAGCTCTTGGT	406
Antropodipase P (membrane-bound)	XPNIPE2	AE10098	Exon3	0	AE10098p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	344	ATGAAAGCCAGCTCTTGGT	407
Antropodipase P (membrane-bound)	XPNIPE2	AE10099	Exon3	0	AE10099p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	345	ATGAAAGCCAGCTCTTGGT	408
Antropodipase P (membrane-bound)	XPNIPE2	AE10100	Exon3	0	AE10100p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	346	ATGAAAGCCAGCTCTTGGT	409
Antropodipase P (membrane-bound)	XPNIPE2	AE10101	Exon3	0	AE10101p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	347	ATGAAAGCCAGCTCTTGGT	410
Antropodipase P (membrane-bound)	XPNIPE2	AE10102	Exon3	0	AE10102p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	348	ATGAAAGCCAGCTCTTGGT	411
Antropodipase P (membrane-bound)	XPNIPE2	AE10103	Exon3	0	AE10103p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	349	ATGAAAGCCAGCTCTTGGT	412
Antropodipase P (membrane-bound)	XPNIPE2	AE10104	Exon3	0	AE10104p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	350	ATGAAAGCCAGCTCTTGGT	413
Antropodipase P (membrane-bound)	XPNIPE2	AE10105	Exon3	0	AE10105p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	351	ATGAAAGCCAGCTCTTGGT	414
Antropodipase P (membrane-bound)	XPNIPE2	AE10106	Exon3	0	AE10106p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	352	ATGAAAGCCAGCTCTTGGT	415
Antropodipase P (membrane-bound)	XPNIPE2	AE10107	Exon3	0	AE10107p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	353	ATGAAAGCCAGCTCTTGGT	416
Antropodipase P (membrane-bound)	XPNIPE2	AE10108	Exon3	0	AE10108p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	354	ATGAAAGCCAGCTCTTGGT	417
Antropodipase P (membrane-bound)	XPNIPE2	AE10109	Exon3	0	AE10109p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	355	ATGAAAGCCAGCTCTTGGT	418
Antropodipase P (membrane-bound)	XPNIPE2	AE10110	Exon3	0	AE10110p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	356	ATGAAAGCCAGCTCTTGGT	419
Antropodipase P (membrane-bound)	XPNIPE2	AE10111	Exon3	0	AE10111p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	357	ATGAAAGCCAGCTCTTGGT	420
Antropodipase P (membrane-bound)	XPNIPE2	AE10112	Exon3	0	AE10112p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	358	ATGAAAGCCAGCTCTTGGT	421
Antropodipase P (membrane-bound)	XPNIPE2	AE10113	Exon3	0	AE10113p8	XPNIPE2_X2f1a	TGGCTCTGTGCCAATAAAGCT	359	ATGAAAGCCAGCTCTTGGT	422

GENE DESCRIPTION	HMC ID	SNP ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)
Bradykinin Receptor B1	BDKRB1	AE10336	Exon3	0	AE10336p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTG	739
Bradykinin Receptor B1	BDKRB1	AE10337	Exon3	0	AE10336p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTG	740
Bradykinin Receptor B1	BDKRB1	AE10338	Exon3	0	AE10336p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTG	741
Bradykinin Receptor B1	BDKRB1	AE10339	Exon3	0	AE10336p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTG	742
Bradykinin Receptor B2	BDKRB2	AE10418	Intron1 or Exon1	0	AE10418p6	BDKRB2_X3.5a	CACCTTGCAGGAAATTTAGTCT	AGAGAGCCCAAGCTCTTGGT	743
Bradykinin Receptor B2	BDKRB2	AE10419	Exon2	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	744
Bradykinin Receptor B2	BDKRB2	AE10420	5' Flank	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	745
Bradykinin Receptor B2	BDKRB2	AE10421	5' Flank	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	746
Bradykinin Receptor B2	BDKRB2	AE10422	5' Flank	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	747
Bradykinin Receptor B2	BDKRB2	AE10423	5' Flank	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	748
Bradykinin Receptor B2	BDKRB2	AE10424	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	749
Bradykinin Receptor B2	BDKRB2	AE10425	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	750
Bradykinin Receptor B2	BDKRB2	AE10426	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	751
Bradykinin Receptor B2	BDKRB2	AE10427	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	752
Bradykinin Receptor B2	BDKRB2	AE10428	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	753
Bradykinin Receptor B2	BDKRB2	AE10429	Exon3	1	AE10418p6	BDKRB2_X3.5a	GGCAGGGCAGGAAATTTAGTCT	AGATCCAGACAGAGAGAGGG	754
Angiotensin Converting Enzyme 2	ACE2	AE10951	Intron14	1	AE10951p28	ACE2_X1.4a	TTTAAACCCAAAGGCAAGG	TTTCTGCTTTTCCAAAGGCT	755
Angiotensin Converting Enzyme 2	ACE2	AE10952	Intron12	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	756
Angiotensin Converting Enzyme 2	ACE2	AE10953	Intron13	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	757
Angiotensin Converting Enzyme 2	ACE2	AE10954	Intron3	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	758
Angiotensin Converting Enzyme 2	ACE2	AE10955	Intron2	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	759
Angiotensin Converting Enzyme 2	ACE2	AE10956	Intron16	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	760
Angiotensin Converting Enzyme 2	ACE2	AE10957	Exon16	1	AE10951p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	761
Protease Inhibitor 4	PI4	AE11081	Intron1	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	762
Protease Inhibitor 4	PI4	AE11082	Exon2	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	763
Protease Inhibitor 4	PI4	AE11083	Intron2	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	764
Protease Inhibitor 4	PI4	AE11084	Intron2	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	765
Protease Inhibitor 4	PI4	AE11085	Intron2	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	766
Protease Inhibitor 4	PI4	AE11086	5' Flank	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	767
Protease Inhibitor 4	PI4	AE11087	5' Flank	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	768
Protease Inhibitor 4	PI4	AE11088	5' Flank	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	769
Protease Inhibitor 4	PI4	AE11089	5' Flank	0	AE11081p22	PI4_X2a	GGACATCTTGATGGGCTCAT	TGGGGCAGCTGTCTTCATAG	770
Antipeptidase P (membrane-bound)	XPNPEP2	AE100524	Intron11	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	988
Antipeptidase P (membrane-bound)	XPNPEP2	AE100525	Intron13	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	989
Antipeptidase P (membrane-bound)	XPNPEP2	AE100526	Intron13	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	990
Antipeptidase P (membrane-bound)	XPNPEP2	AE100527	Intron7	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	991
Antipeptidase P (membrane-bound)	XPNPEP2	AE100528	Exon21	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	992
Antipeptidase P (membrane-bound)	XPNPEP2	AE100529	Exon21	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	993
Antipeptidase P (membrane-bound)	XPNPEP2	AE100530	Exon6	0	AE100524p46	XPNPEP2_X1.2a	TTTCAAGGCTGACATCTCTG	TGGAGTGTCTGCTGCTTACG	994
Bradykinin Receptor B1	BDKRB1	AE103310	Exon3	0	AE103310p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	995
Bradykinin Receptor B1	BDKRB1	AE103311	Exon3	0	AE103310p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	996
Bradykinin Receptor B1	BDKRB1	AE103312	Exon3	0	AE103310p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	997
Bradykinin Receptor B1	BDKRB1	AE103313	Exon3	0	AE103310p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	998
Bradykinin Receptor B1	BDKRB1	AE103314	Exon3	0	AE103310p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	999
Bradykinin Receptor B2	BDKRB2	AE104330	Exon3	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1000
Bradykinin Receptor B2	BDKRB2	AE104331	Exon3	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1001
Bradykinin Receptor B2	BDKRB2	AE104332	Intron1	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1002
Bradykinin Receptor B2	BDKRB2	AE104333	Intron1	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1003
Bradykinin Receptor B2	BDKRB2	AE104334	Exon3	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1004
Bradykinin Receptor B2	BDKRB2	AE104335	Exon3	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1005
Bradykinin Receptor B2	BDKRB2	AE104336	Exon3	1	AE104330p28	BDKRB2_X3.7a	GGATATCTTTCAGAGGGGATC	TGCACGCTGTCACTATACCT	1006
Protease Inhibitor 4	PI4	AE110810	Exon4	0	AE110810p30	PI4_X4a	ATTTCTGCTGCTGCTGCTGCT	CTTTCAGAGGGGCAACTT	1007
Protease Inhibitor 4	PI4	AE110811	Exon4	0	AE110810p30	PI4_X4a	ATTTCTGCTGCTGCTGCTGCT	CTTTCAGAGGGGCAACTT	1008
Protease Inhibitor 4	PI4	AE110812	5' Flank	0	AE110810p30	PI4_X4a	ATTTCTGCTGCTGCTGCTGCT	CTTTCAGAGGGGCAACTT	1009
Bradykinin Receptor 1	TACR1	AE10658	Intron4	1	AE10658p10	TACR1_X4a	ATTTCTGCTGCTGCTGCTGCT	CTTTCAGAGGGGCAACTT	1010
Bradykinin Receptor 1	TACR1	AE10659	Intron3	1	AE10658p10	TACR1_X4a	ATTTCTGCTGCTGCTGCTGCT	CTTTCAGAGGGGCAACTT	1011
Angiotensin Converting Enzyme 2	ACE2	AE10958	Intron13	1	AE10958p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	1012
Angiotensin Converting Enzyme 2	ACE2	AE10959	Intron6	1	AE10958p30	ACE2_X1.3a	CACCATAGCAGAGAAAGAGCA	GCCAGAGTCAAGAGAAAGAAC	1013

[illegible]

Table IX (2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	Target_Name	Forward sequencing primer	Forward sequencing primer (SEQ ID NO:)	Reverse sequencing primer	Reverse sequencing primer (SEQ ID NO:)
Brahylin Receptor B2	BDRB2	AE10428	Exon3	1	BDRB2_X3-2a	TTCCTGAGACAGGAACAGTCC	785	TATTCGACACATCTGTGTCG	817
Brahylin Receptor B2	BDRB2	AE10429	Exon3	1	BDRB2_X3-2a	TTCCTGAGACAGGAACAGTCC	786	TATTCGACACATCTGTGTCG	818
Angiotensin Converting Enzyme 2	ACE2	AE10941	Intron14	1	ACE2_X14a	TTTGTGAGACAGTGTGGAGGATA	787	ATGTGGGATCTTTGGAGGATA	819
Angiotensin Converting Enzyme 2	ACE2	AE10942	Intron13	1	ACE2_X13a	TTTGTGAGACAGTGTGGAGGATA	788	ATGTGGGATCTTTGGAGGATA	820
Angiotensin Converting Enzyme 2	ACE2	AE10943	Intron3	1	ACE2_X3a	CAGCTGTGTGCACAGTGCCTCA	AE10931	ACATCTGGACAGCCCTCAAAAG	AE10932
Angiotensin Converting Enzyme 2	ACE2	AE10944	Intron3	1	ACE2_X3a	CAGCTGTGTGCACAGTGCCTCA	AE10931	ACATCTGGACAGCCCTCAAAAG	AE10932
Angiotensin Converting Enzyme 2	ACE2	AE10945	Intron18	1	ACE2_X18a	TCTATCTCTCTGTGCCCTTTA	AE10937	TCTATCTCTCTGTGCCCTTTA	AE10937
Angiotensin Converting Enzyme 2	ACE2	AE10946	Intron18	1	ACE2_X18a	TCTATCTCTCTGTGCCCTTTA	AE10937	TCTATCTCTCTGTGCCCTTTA	AE10937
Angiotensin Converting Enzyme 2	ACE2	AE10947	Intron16	1	ACE2_X16a	GGATCACTGGAGACACACACA	AE10939	CTCTCCGCTGATCTGCTATTC	AE10940
Angiotensin Converting Enzyme 2	ACE2	AE10948	Intron16	1	ACE2_X16a	GGATCACTGGAGACACACACA	AE10939	CTCTCCGCTGATCTGCTATTC	AE10940
Protease Inhibitor 4	P4	AE11041	Intron1	0	P4_X1a	GATCTGGAGGACATGTTCTTG	AE11023	CACATGTATAGCTGTGCGG	AE11024
Protease Inhibitor 4	P4	AE11042	Intron2	0	P4_X2a	GATCTGGAGGACATGTTCTTG	AE11023	CACATGTATAGCTGTGCGG	AE11024
Protease Inhibitor 4	P4	AE11043	Intron2	0	P4_X3a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11044	Intron2	0	P4_X3a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11045	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11046	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11047	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11048	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11049	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Protease Inhibitor 4	P4	AE11050	Exon1	0	P4_X13a	CTTCCACATCACTTTGCTGG	AE11027	ATTTTGATAGCTGCAGTTT	AE11028
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10044	Intron11	0	XNPDP2_X12a	ATCTGCACTGCTGGGTGTGGCT	804	ACCGAAGAAGCTGTCTACTCTG	1040
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10045	Intron13	0	XNPDP2_X13a	AGTTTGAGAGGTGTAGAGCAGCG	AE10061	GCACACTTCGCTACTCCACACTGT	AE10052
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10046	Intron13	0	XNPDP2_X13a	AGTTTGAGAGGTGTAGAGCAGCG	AE10061	GCACACTTCGCTACTCCACACTGT	AE10052
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10047	Intron7	0	XNPDP2_X7a	AGAGTGTTCGAGTCTGTGTTTAG	1017	CTTACCGCTCTTGTGTTCGTCG	AE10053
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP2_X21.14a	CAATGCTGTTTAAGTCTTCCGCA	1018	CTACCGCTCTTGTGTTCGTCG	AE10056
Antropodiosin 2 (membrane-bound)	XNPDP2	AE10049	Exon21	0	XNPDP				

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:1)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:1)	ORCHID_SNPLT	ORCHID_SNPLT (SEQ ID NO:1)
AE100s1	TATCATTTGTCCTATGACCG	1066	CAGGTCAGGAGAGCC	1154	CCTCATGATGTCGCTGCTGCTCC	1242
AE100s10	AAACTTCATCATCAGAGTACCAAG	1067	GAGGACATTTTGATTCAGACTCCTC	1155	GTGGTTTGCAAACCTTACATGCAC	1243
AE100s11	ATAGAATGACTTCTCCAGAGGGA	1068	CAGCTTAACCTGTAATGCGG	1156	TGGAAGCCAGCCAGGAGGT	1244
AE100s12	TCCAGAGGACTGCGCTG	1069	GAAGGAGAGCTTAACCTG	1157	AGCCAGGCCCCAGAGGTCTCCCA	1245
AE100s13	ATAGAATGACTTCTCCAGAGGGA	1070	GCTGAGAGGAGGAGAGATGTT	1158	AATGTCAGANGNCAGGCTTAACCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCTCTGTCTGCTGAG	1071	GATGAGGAGCAAGGGAG	1159	CCGSGCTCTCTCTCANGCNTTTCT	1247
AE100s16	AAAGAAGAGAGAGAGAGAGAA	1072	GTGTAGGAATAGAGAGGGGTATAGG	1160	AGAAAGCTTGCTCAGGAGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGAGAGCCCTCTCA	1073	GATCCAGAGCATCTCTATGAGC	1161	TACTTAATTAATTAATTAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATTTGAGGGGAGGG	1074	GTATCTTTTGAGGTTCACTCCCC	1162	GCAACAAGTCTCTCTTNCAGAACAGTC	1250
AE100s20	TACCACAGAGGGGACTGG	1075	GATTGAGTACTGAGGCTGG	1163	AGACTTCACCTCTTGCCANCTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCTTANGCAGACAAATTT	1076	GAGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGGTGAAGA	1252
AE100s24	CGCTATCTGATCTCCATCATCT	1077	CCGCACCTGGAGTTGGGG	1165	TTNGAGGCTGTGGCTNCAACAGACCT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGATTTGTTGAGGAAGG	1078	GAGCCCCAAAAGTGTATGTA	1166	TTACCTTANGGCTGACCTNCCAGGAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTCTTTCAGTTGGCACCA	1079	CAATGGAGAGAGGAGGGG	1167	TCACCTGGCTCTCTCAGGAGTCC	1255
AE100s4	TCCCTGCTGCTTCCCGG	1080	AATATTTGTGCTGATTTACAGATAG	1168	TATTTGAGNCCACTGACAGGCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGATGATGAGGTAGGTG	1081	CTTTGCTATTTTCATCTCTGTGAAA	1169	ACCTTCATGAGGGGTATTAATAAG	1257
AE100s7	ATCCAGTAATGGCAAGCCNG	1082	GTGAGCTTTAGGTAACAGTTTGG	1170	AAGAGTTTGTGTTGAGGAAGGGTTT	1258
AE100s8	GCAATCTCAGCTGCTG	1083	CAGGTCTGGGGGCAAGTA	1171	GTAAAGAGGGTCTONATNCAACAGGGG	1259
AE100s9	AAACTAGAGAGACAGAGAGCAC	1084	TTTCAGAGACTGGCAGGAG	1172	CACAGCTAGAGAGATTCACAGAAA	1260
AE103s1	AACTTCTTTGCTTCACTAACAGCT	1085	GATGAAGATATTTGAGCAAGACTTTTAG	1173	CCAGTAATTTATGCTCTTTTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGATCTTACCAATT	1086	GACTCTGAGCTCTCTGCTC	1174	ATCCTGAATATATCCAAAGTGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACCGAGTTTCTGTAATTTG	1087	CTTTGAATGACAAATGGAGTGTATAGA	1175	CAGCAGGAACAAATAACAGTATC	1263
AE103s14	TGTATAGCAGCAGCAGGAA	1088	CCTGCGAGTTAGCTAGAAAGC	1176	ACAAGTATCGGTAAATGCTCTCTTA	1264
AE103s2	TGACAAATGCTCAGAGCC	1089	CAACAGGACAAAGAGTTCC	1177	CTGGAGCTCTGCTAGCAGAGTCTGCC	1265
AE103s3	ACTTTCTGCGGGAATTAAACA	1090	ACCCGCCATCTACGGGA	1178	TGAACCAANAGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGAGAGAAATATCTGA	1091	CCACGAGAGATGCTGATG	1179	GAGCCCTCTCTGCGGTGTATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGACATCACCGCT	1092	GTAGTTGAGAGAGACATCGC	1180	AGATCTGAACATCACCGGCTGCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGAGCAATATGCTGTTTTTGATAA	1093	CTCACCTGCTGCTGTTG	1181	CACTGGGCAATGNGGCGCTCCGCC	1269
AE104s10	GTTGGGCGCTCAGGGTG	1094	GTGGCGGTGTGAGCACCC	1182	GTNGAATGACAGGTGGAAGGAGCCA	1270

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:1)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:1)	ORCHID_SNIPPIT	ORCHID_SNIPPIT (SEQ ID NO:1)
AE104s11	TTGAGTGTGAATGCTTCTCTG	1095	GCCCTATGATGATGATGATG	1183	TTACACATACACAGCNCATTTAGTCTT	1271
AE104s12	ATTTTCTCTTTGGATGTGAATG	1096	GGGCCCTATGATGATGATG	1184	TAACAGCTCATTTAGTCTTTCACAG	1272
AE104s13	GCCATTTGGCGGAGAGCTC	1097	AAAAAAGAGGCTGTGTTTGTCA	1185	GGCAGTCAATTCAGACACAGAGCAC	1273
AE104s14	AAGTGAATGATGCTGCCCT	1098	AAGTGGCCCATGATGAGC	1186	CCCTAGAGAGGTGCAAAAGGAATG	1274
AE104s16	GATGATGATGATGATGATG	1099	CAGTATGGGAATTTCAATATCC	1187	ATTCCTTCACTCATTTATATNAACAAAA	1275
AE104s17	GATGGAACAGATGAAGAGAGG	1100	CATTAATGCCCTCTCTCCAT	1188	TACGTTGAGGATGAGCCCGAGTT	1276
AE104s18	AGAGAAAGATGTTAGATGCA	1101	CATTGATGAGGAGATGATG	1189	ACAGGCTGGGATGATGATGATACAC	1277
AE104s21	TAACCTAGTAACATGAGGAATCCCTTT	1102	CACTCTGATGCAAAATGTTCTTC	1190	GTGCTGGGACGAGTGTCTCAC	1278
AE104s2	GAGGCAATTAATGCTGTTTTTGTATAA	1103	CTCACCTGTGCTGCTGTG	1191	GTACAGGAGGGGNCACCTGGCGCGG	1279
AE104s20	TTTACACTCCAGGCGCTGAG	1104	CTCTTCCAGATCCACTGG	1192	TTTTTGNAGCTTTAAACACCTTCCTTC	1280
AE104s21	GGATTTCTTTGTATGCAAGTAC	1105	CATCATCTCCGAGGAACGG	1193	GCAGAAGCTGTCTCTTTCTCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGAGTGGCGGCG	1106	GCAGGATGAGAGCTCAG	1194	GAAGTCCCGAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTAAGAAACCCAGGG	1107	GTCTCTGCTCTCTGCCCC	1195	CATTGACCAACAACTGGATGCG	1283
AE104s27	TCGACCTCTCTCGTCGAAC	1108	GAAGAGAGAGGACCATCTCCA	1196	GCTTTGAGTGTGTCAGTGGCCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s30	TTTGAAGGAGGGAATC	1109	CAACCTGCACTCCAGC	1197	GAGCGAAGGCTGCTGATGATGATG	1285
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGATACATGCTAGGAGCT	1110	GTCTGGACCCCAATGTTCTAT	1198	ACCTTTGCTTCAATTTTCACTGTA	1286
AE104s34	ACACTGGTCTTCAACCG	1111	GTACATGTGAGGATCATTAGC	1199	GGCTCCCAATGATGATGCTGCTCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCTGCTGCTCATCA	1112	CATCTTGAAGAACTCAAGATCA	1200	ACCACAGCACCTGCTGACGCTCTC	1288
AE104s4	AGTGAAGCTTGGATGCA	1113	CTTTGATGAAAGAGGAGCA	1201	AGGTTGAGGAGAGCTGGATGAGG	1289
AE104s5	TGCAAGGTTGCAAGGAGA	1114	CAAGAGAGGCTCTTTGGAT	1202	GCTGGGATGATGCTGGGCTGCTCT	1290
AE104s6	GGCTCAACACTGTGGAATGTC	1115	CAAGAGGCTGCTGCTG	1203	GTCTCTGGAAGAAACACTGTGCTG	1291
AE104s7	AACCTGTGGCCAGAGGT	1116	AACCTTACCCACACG	1204	CCCCCTCTCCAACTGCTGCTCCACAA	1292
AE104s8	ATGTAGCTAGCACCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGGGGAACTGAGGCGGAGCAG	1293
AE104s9	TATTTCTAGACTCAGTCTTTTCTTATAG	1118	GAAGTCTGCTGAGGTTAAGG	1206	AAGGTCTCTAGCTATATGAGGATC	1294
AE105s1	GAGAGACTCTGAGGGGG	1119	AGGTCTTCACTGCTCTGCA	1207	CCAGGCTGAGGGAAGAAAGGACA	1295
AE105s2	ATTGTGACAGAGGGTGGG	1120	CAAACTCAGATTTGGAGGC	1208	GAGATCGGTAGAGAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	CCGAAGGGAAGGTGCGAA	1121	TTGAGTTGGTTGCGCAA	1209	AAGCTGAANCTGNAAGATGGGTTCA	1297
AE105s5	TGTTGGGGATGCTTTGG	1122	GATGCTGAATGGGAAAGG	1210	AAGCTTACCACGCTTCTCAG	1298
AE105s6	ATCTCTGGCCCGCAC	1123	CATATCTGCTCCCATGAGAC	1211	GGAATCTTGTCTGCTGCTCCAGACA	1299
AE106s1	TATCAAGGCCACAGCCG	1124	CACACGAATGATGATGAGC	1212	TACTGGGAGAGACAGCGGATGGG	1300
AE106s2	ATGCTCTCTGTTGATGATGATG	1125	CATCATACATCCCTCCAGC	1213	CCAGCAGAGAGACGAGGACCA	1301
AE106s3	ATGCTCTCTGTTGATGATGATG	1126	CTACAGGAGCAAGTCTCTG	1214	CCAAGCGAGGTGAGCAGGGG	1302
AE106s4	TGCAGATTCATCTGAAATGA	1127	CTGCTGACTCAACCAATCACT	1215	AGGTGGACCACTTTTCCCAA	1303
AE106s5	AAAAGCTGCTCGACCTTTTAT	1128	TCAAACTCTCAATCTTCTCTATCT	1216	TCCCTATCTTTGACNCTTATGCTGT	1304
AE106s6	TTGAGTGCACAGATGAGG	1129	CATGGAATCTCTTCTATCTG	1217	ACCATACTGACCTTTTTCAGTGC	1305
AE106s7	ATGCTCTTGGATCATTCTG	1130	CCACGAGAGGAGCCAG	1218	AGAGCATGTGAGGCTGAGTNCAGGGA	1306

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNIPIT	ORCHID_SNIPIT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTCGAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAAGTGTGTGCAC	1219	CAAAATCTGCTCCCTAATGATGAGTGC	1307
AE107s2	AGCATCGAACACAGAAATTGTATG	1132	CTTCCCTGGCCCTTTCTC	1220	TCCTCTTGACRCAGGAGTCCCATCCC	1308
AE107s3	CCCTGCTGATCATTACACAGATG	1133	CATACAAATTTCTGTGTTGTGATGC	1221	GCTGTGAAGTTCGCGGAGTTGCCACCC	1309
AE107s4	ATCGACACAGAAATTGTATGTGG	1134	GGGAGAAAAGGGCTGCA	1222	AAGCGGGGATGGGAGCTCTCTG	1310
AE107s5	ACCTGGACCCACTCGCT	1135	CTTTTCCCACTCGCTG	1223	TGNGGCCACCCAGCTGTCTCA	1311
AE107s6	CCAGTAAATCAAAATGTGCATCC	1136	CAGCTCAGCCGAGTGGG	1224	ATGTGTGTCACTGTTCTGCAATCACCC	1312
AE109s1	AATAGCTTATCAATAAGGAATAGGTTACTTT	1137	GAATTGATTTATTTTGTAGTGCACAGTC	1225	ATCTGGAACCTTATAGTNTTTGAAAAGAA	1313
AE109s2	GGGGGTTCAAGGCCCTTTT	1138	GCAAAATTTAGCCAGTCAAAAGCA	1226	GAGGGTTCCAGGANGTACNTATATTTTA	1314
AE109s3	TGGGGCCAAAGGAGTAG	1139	GCTGAAGACACAGACAGATTC	1227	AAGTAGACAGGAATGGGTGTGAAA	1315
AE109s4	GTGTGAAACACACATATCTGCAAT	1140	TGGAAAAGTTTGTAAACCCAGATATC	1228	TCATAATCACNVNTNAAANTTAGTAGC	1316
AE109s5	GTGTTCACCTGCAAAATTAAGATAATAACA	1141	ACATGGCAAGAAGTAATTTGCTG	1229	GAATTTTGTCTGAAGAGATCTCTAA	1317
AE109s6	AACTCRAATCAAGATTATTCCTCCCTG	1142	GTTCACCAATACACACAACTAACCACTATT	1230	CACATGTAAATGATCTCAGAAATAATG	1318
AE109s7	CCCTCACCTTAGATGAAAGTAAAA	1143	TTTGAAACCAAGAAATCTCTTTAAATTT	1231	TTCAAGTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCTCTCCCTGCTCATTTG	1232	CTTGTAAANAAGCCCAATNAATTTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGGATGAG	1145	ATGTGGCGATTGGTCTGG	1233	GGNTGGCACCGAGNTGCCAGAGCCAC	1321
AE110s11	CACCTCTGCACTCTCTCA	1146	CATGGTGTCAATTCAGGAATTTTG	1234	AACTCTNCCGNCATGGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAACTGG	1147	CAGTAGAATGCTTTTGTATTTTACC	1235	TNTCTTGGACAGATCTTNTATTTGAAA	1323
AE110s2	CTGTACCTTTTTCATCTTCCCTT	1148	GCAGCATCATGGGCACCC	1236	CCGGACTGNTGTGTCTCTCATCAACATA	1324
AE110s3	AAGGNGGCTCTGCCAG	1149	GATGCACTCTAGCTTCTGTGTAATAATTT	1237	GATCTGCTGTTGTTCTANTANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAAGCACCGTCAAGAA	1150	GATTTAGCATATACCAATGATCTGACTCT	1238	GAGGAAGATTTGTGATTTGTTGTCAG	1326
AE110s6	GTCAAACTTAATGCTGAAAGTGG	1151	TTTCAGATGAGTTGATTTTCATTAGTGC	1239	AGACCTTAAATAATAAATCTCTGAGGAT	1327
AE110s7	AGGGTCAAACTAAATAGGCTGAAA	1152	CACCTTGTCTTTTCAGATGAGTGTGATTTTC	1240	TAAACCATATATAAGACATCTCCACAGA	1328
AE110s8	AGAACTGGAGTATCTTTCTTGGG	1153	CTGTAGAGGTCTAGTAGACTGTGCTTTTG	1241	TATGAAGCGGTACCACTTCTATCCCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO.1)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO.1)
AE100s1	TGTAATAACGACGGCCAGTAGTTCCTCCTCCCTCCCTCACT	1330	CAGGAAACAGCTATGACAGGAAGCTCTGGGGTCTC	1451
AE100s10	TGTAATAACGACGGCCAGTGCGGACATCAGGTATATTCAGT	1331	CAGGAAACAGCTATGACAGCCACGCGCAGCAATTC	1452
AE100s11	TGTAATAACGACGGCCAGTTCCTGGGCTTTATACCTCTCTC	1332	CAGGAAACAGCTATGACAGAGGTCTGCGAGAGACAC	1453
AE100s12	TGTAATAACGACGGCCAGTTCCTGGGCTTTACCTCTCTC	1333	CAGGAAACAGCTATGACAGAGGTCTGAGGACAGACAC	1454
AE100s13	TGTAATAACGACGGCCAGTTCAGGCTCAGAGATTAACAGAC	1334	CAGGAAACAGCTATGACAGAGGTCTGCGAGAGACAC	1455
AE100s14	TGTAATAACGACGGCCAGTACAGACTTGCACAGCTCG	1335	CAGGAAACAGCTATGACAGTACGACATACACAGACAG	1456
AE100s15	TGTAATAACGACGGCCAGTCTTCCATCTATCACAAG	1336	CAGGAAACAGCTATGACCACTGACATACATACACAGAG	1457
AE100s16	TGTAATAACGACGGCCAGTCAGTGAGATCTTTGCCACTGC	1337	CAGGAAACAGCTATGACCCACAGCTTAGGAAAGGCC	1458
AE100s17	TGTAATAACGACGGCCAGTCCACACCTTATCATCAGG	1338	CAGGAAACAGCTATGACCTGTGCTCTCTCTGAAATCT	1459
AE100s18	TGTAATAACGACGGCCAGTTATCCAGGATAGGTGGCATGT	1339	CAGGAAACAGCTATGACCACTAGCGATGTGTGTGGAG	1460
AE100s19	TGTAATAACGACGGCCAGTCAGAGGGAGACGTGTGATG	1340	CAGGAAACAGCTATGACCTTGTCTGTGTGAAACCC	1461
AE100s2	TGTAATAACGACGGCCAGTTGTAAAGCCCTTTGCGAGAT	1341	CAGGAAACAGCTATGACCTTGTCTGTGTGTGAAAGCC	1462
AE100s20	TGTAATAACGACGGCCAGTCTCTGAAAGCCCCAGAGAT	1342	CAGGAAACAGCTATGACCTTGTGTGAAGCCACTCGA	1463
AE100s21	TGTAATAACGACGGCCAGTGGGCTCCAGACTCTCTGTT	1343	CAGGAAACAGCTATGACCGGAGAGCTGTGTAGCACT	1464
AE100s22	TGTAATAACGACGGCCAGTCACTGCTTAGAAGACCTTTGCA	1344	CAGGAAACAGCTATGACCACTTGTCTCTCTGGGGTT	1465
AE100s23	TGTAATAACGACGGCCAGTAGGACACAGCTACATGCTGTT	1345	CAGGAAACAGCTATGACCACTGTGCAATCCAGAGCAAT	1466
AE100s24	TGTAATAACGACGGCCAGTCTGCCCTCAACAGACACTCT	1346	CAGGAAACAGCTATGACCGCACTTTGTCTCCAGACTT	1467
AE100s25	TGTAATAACGACGGCCAGTAGAAGAACAGTTCTCTCCCGG	1347	CAGGAAACAGCTATGACCCCACTGTGAACTGTGTGAG	1468
AE100s26	TGTAATAACGACGGCCAGTCACTCTGCTCTGCTTTGACTTC	1348	CAGGAAACAGCTATGACCGGCAACTCTCTCTACTTCCA	1469
AE100s27	TGTAATAACGACGGCCAGTCACTGAGTACAGAGGGGTATGG	1349	CAGGAAACAGCTATGACCGCTCTGCAATTCACACAT	1470
AE100s28	TGTAATAACGACGGCCAGTGGGTGTATATACACACCTCTGG	1350	CAGGAAACAGCTATGACACAGACACCAATTTCTTATG	1471
AE100s29	TGTAATAACGACGGCCAGTTCGAGATATGAAAGCCAGCTAG	1351	CAGGAAACAGCTATGACCGCTTCTCCAACTCTGGT	1472
AE100s3	TGTAATAACGACGGCCAGTCTGTGGAAGAACAGACAGAC	1352	CAGGAAACAGCTATGACCTGTGTCAGGCTGTGGAAT	1473
AE100s30	TGTAATAACGACGGCCAGTACGAAATTTAGGCGCATCACT	1353	CAGGAAACAGCTATGACCCCTCTTCTGTACCAAGCT	1474
AE100s4	TGTAATAACGACGGCCAGTAGCAGTCAAGATCCCTTCCAT	1354	CAGGAAACAGCTATGACCTTTCTGTGAACACCTCT	1475
AE100s5	TGTAATAACGACGGCCAGTGAAGAGCCCTCCCTCTCTC	1355	CAGGAAACAGCTATGACCTTTGCAATTCGGGTAGTCT	1476
AE100s6	TGTAATAACGACGGCCAGTCAAGGTGGACAGCTTTCCGTA	1356	CAGGAAACAGCTATGACCTCTGTGCAATTTCTCTAC	1477
AE100s7	TGTAATAACGACGGCCAGTCTCTATAGCACGCCCTATTGTA	1357	CAGGAAACAGCTATGACCGGACGCCAGCTACTTTTC	1478
AE100s8	TGTAATAACGACGGCCAGTATCCGAGACAGCGAGGTTCAT	1358	CAGGAAACAGCTATGACCTGTCTCTACTGCTCTCT	1479
AE100s9	TGTAATAACGACGGCCAGTATTCGGAAGACAGCGAGTTCAT	1359	CAGGAAACAGCTATGACCTGTGGGAGTAGGTGTCTG	1480
AE103s1	TGTAATAACGACGGCCAGTCTTTGCTCTCTCTGCAATTTCT	1360	CAGGAAACAGCTATGACCTCAATGCTGTCTTTTAATTT	1481
AE103s10	TGTAATAACGACGGCCAGTGTGCCAGATCTGAAACATCAC	1361	CAGGAAACAGCTATGACCGCACTGTCTGTGACACTCGA	1482
AE103s11	TGTAATAACGACGGCCAGTCCCAAGAGTCTGGCTTTTC	1362	CAGGAAACAGCTATGACCTTAATCTTTTCTCTCTCTG	1483
AE103s12	TGTAATAACGACGGCCAGTACTTCCAGACTCAAGGGAT	1363	CAGGAAACAGCTATGACCTCTCTGTATTTCTCTGGCA	1484
AE103s13	TGTAATAACGACGGCCAGTCAAGTCACTCCACTTTTGGT	1364	CAGGAAACAGCTATGACCTGTGTGTCTCATGCAAT	1485
AE103s14	TGTAATAACGACGGCCAGTCTTCACTTTGCTTCTCCCTA	1365	CAGGAAACAGCTATGACCTGTGTGTCTCATGCAAT	1486
AE103s2	TGTAATAACGACGGCCAGTGTCTGTAGTCTGCCACTCTG	1366	CAGGAAACAGCTATGACCGATTAATTTCTCTGCCCAAG	1487
AE103s4	TGTAATAACGACGGCCAGTCTCGGAACACAGACCAATTAA	1368	CAGGAAACAGCTATGACCAAGGACAGATGATCATGAC	1489
AE103s5	TGTAATAACGACGGCCAGTCTTCCAGACTCAAGGGAT	1369	CAGGAAACAGCTATGACCTCTCTGTATTTCTGGGCA	1490
AE103s6	TGTAATAACGACGGCCAGTCTTCTTGGGCAAGAGATATC	1370	CAGGAAACAGCTATGACCTGTGTGTGTAGGAGGAAACC	1491
AE103s7	TGTAATAACGACGGCCAGTCTTCTTGGGCAAGAGATATC	1371	CAGGAAACAGCTATGACCTGTGTGTGTAGGAGGAAACC	1492
AE103s8	TGTAATAACGACGGCCAGTGCATCTCTCTTGGTGGTG	1372	CAGGAAACAGCTATGACCTCTGTGGTCTTGTCTATCC	1493
AE103s9	TGTAATAACGACGGCCAGTGTCTCCAGATCTGTGAACATCAC	1373	CAGGAAACAGCTATGACCAAGATTTCTCCAGAGGCA	1494
AE104s1	TGTAATAACGACGGCCAGTGTGTCTTTTAAGAGAGGCTCT	1374	CAGGAAACAGCTATGACCGCACTTTTGTGCACCAAGC	1495
AE104s10	TGTAATAACGACGGCCAGTGTGTCTTGTGTGTGTGTGTCTCT	1375	CAGGAAACAGCTATGACCGTGTGTGTGTGTGTGTGTGT	1496

AE104s11	TGTAAACGACGGCCAGTTCGGGAGTTGTAAACAAATGCT	1376	CAGAAACAGCTATGACCGAGGCTGTGTTTGTCA	1497
AE104s12	TGTAAACGACGGCCAGTTCGATGCAAAACCTCATCCA	1377	CAGAAACAGCTATGACCGAGGCTGTGTTTGTCA	1498
AE104s13	TGTAAACGACGGCCAGTTCATACCAATGCATAGGCG	1378	CAGAAACAGCTATGACCTGGAGGAGAAACAGG	1499
AE104s14	TGTAAACGACGGCCAGTTCAGCTCTCCAGCTTAGGCC	1379	CAGAAACAGCTATGACCAATTCCTTAATTCGGTCTTG	1500
AE104s16	TGTAAACGACGGCCAGTTCATAAAGAGGTCTGACCCAC	1380	CAGAAACAGCTATGACCTTAGACTAGATCATAGGGCCA	1501
AE104s17	TGTAAACGACGGCCAGTTCACCATGACCCAAAGTTTAT	1381	CAGAAACAGCTATGACCGCCACTTGTTCATCTACT	1502
AE104s18	TGTAAACGACGGCCAGTTCAGGAAATCCCTTTGACTCAC	1382	CAGAAACAGCTATGACCGACTGAGCAATGTCTGG	1503
AE104s19	TGTAAACGACGGCCAGTTCCTTCAACTGTGTGCC	1383	CAGAAACAGCTATGACCAACCAACGCTCCATTTGAGT	1504
AE104s2	TGTAAACGACGGCCAGTTCGTGCTTTAAAGGAGGCGTG	1384	CAGAAACAGCTATGACCGACTTTTGGACCAACCG	1505
AE104s20	TGTAAACGACGGCCAGTTCATGATGCGGAGGTTTCT	1385	CAGAAACAGCTATGACCGCCCAATATAAACTGAT	1506
AE104s21	TGTAAACGACGGCCAGTTCATGATGAAACAGTGGCG	1386	CAGAAACAGCTATGACCTTGCAGCAAACTGACCA	1507
AE104s22	TGTAAACGACGGCCAGTTCAGTCCCTCTGCTGATTAAT	1387	CAGAAACAGCTATGACCTTGCAGCAAACTGACAA	1508
AE104s23	TGTAAACGACGGCCAGTTCAGTCCCTCTGCTGATAC	1388	CAGAAACAGCTATGACCAATGCAAAATCTTTCGCA	1509
AE104s24	TGTAAACGACGGCCAGTTCATCTGATGATGGGTCTG	1389	CAGAAACAGCTATGACCAAGATGCGAGAATTC	1510
AE104s25	TGTAAACGACGGCCAGTTCAGTCACTGCTCTCAATCCT	1390	CAGAAACAGCTATGACCTTAATCAACAGATCGCC	1511
AE104s26	TGTAAACGACGGCCAGTTCCTCTGCTCAATCATGTA	1391	CAGAAACAGCTATGACCTTCCAGGACTTCCAAATC	1512
AE104s27	TGTAAACGACGGCCAGTTCCTCTCAATCATGATGTT	1392	CAGAAACAGCTATGACCTTCTGATGGACAAGGA	1513
AE104s28	TGTAAACGACGGCCAGTTCCTCTCAATGCTCTCTGTG	1393	CAGAAACAGCTATGACCGGTGATATGGACAGCA	1514
AE104s29	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTC	1394	CAGAAACAGCTATGACCTTATGCAATGTTGA	1515
AE104s3	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1395	CAGAAACAGCTATGACCGGAACTCAAGACTCAA	1516
AE104s30	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1396	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1517
AE104s31	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1397	CAGAAACAGCTATGACCAATCCATATTTACACCA	1518
AE104s32	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1398	CAGAAACAGCTATGACCAATCCATATTTACACCA	1519
AE104s33	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1399	CAGAAACAGCTATGACCAATCCATATTTACACCA	1520
AE104s34	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1400	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1521
AE104s35	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1401	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1522
AE104s36	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1402	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1523
AE104s4	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1403	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1524
AE104s5	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1404	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1525
AE104s6	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1405	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1526
AE104s7	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1406	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1527
AE104s8	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1407	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1528
AE104s9	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1408	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1529
AE105s1	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1409	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1530
AE105s2	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1410	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1531
AE105s3	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1411	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1532
AE105s4	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1412	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1533
AE105s5	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1413	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1534
AE105s6	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1414	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1535
AE106s2	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1415	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1536
AE106s3	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1416	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1537
AE106s4	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1417	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1538
AE106s5	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1418	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1539
AE106s6	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1419	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1540
AE106s7	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1420	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1541
AE106s8	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1421	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1542
AE106s9	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1422	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1543
AE107s1	TGTAAACGACGGCCAGTTCCTCTCAGCACTGTGATCCTCA	1423	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1544
		1424	CAGAAACAGCTATGACCTTGAATGAAAGAGGA	1545

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AE107s2	TGTAATAACGACGGCCAGTCTCTGACAGAGCCTGCTGATAC	1425	CAGGAACACGCTATGACCATTTTGAGGTCCACACA	1546
AE107s3	TGTAATAACGACGGCCAGTCCAGTTTGTTCATGTCAGT	1426	CAGGAACACGCTATGACCGGAATAAGAGCTACGAA	1547
AE107s4	TGTAATAACGACGGCCAGTCTCTGACAGAGCCTGCTGATAC	1427	CAGGAACACGCTATGACCAAGTCTGTCTACCTCTGTG	1548
AE107s5	TGTAATAACGACGGCCAGTCCCTTACCCCTAGTAATAATCAA	1428	CAGGAACACGCTATGACCACTCTCTCAGCCTCAGAC	1549
AE107s6	TGTAATAACGACGGCCAGTCCCTGCTGAGTCTGCTTAT	1429	CAGGAACACGCTATGACCTCTGTCTGTCTGCACTGTG	1550
AE109s1	TGTAATAACGACGGCCAGTTCAGCAGAGTCAATTGAAGGA	1430	CAGGAACACGCTATGACCATGACAGCAACCAAGCATC	1551
AE109s2	TGTAATAACGACGGCCAGTCAAAAGTGTGACGAGTGGCC	1431	CAGGAACACGCTATGACCGACCATACACAAATTGG	1552
AE109s3	TGTAATAACGACGGCCAGTAAATGCGAGCTGTCAACATAG	1432	CAGGAACACGCTATGACCAATGATGTGTAAGGCGA	1553
AE109s4	TGTAATAACGACGGCCAGTTCGACAGAAAAATAAACCACTGA	1433	CAGGAACACGCTATGACCTCTTTCAGCAAAATTTCC	1554
AE109s5	TGTAATAACGACGGCCAGTGCATTTCTGTGATTAATCTGGG	1434	CAGGAACACGCTATGACCTCGACAGTGGGAAACT	1555
AE109s6	TGTAATAACGACGGCCAGTGTGCTCCCATAGTGGTAACCTGC	1435	CAGGAACACGCTATGACCTCCCTCCCATGTCTCTCT	1556
AE109s7	TGTAATAACGACGGCCAGTGCACACAGGAAGAACACACAA	1436	CAGGAACACGCTATGACCTCCCTCCCATGTCTCTCT	1557
AE109s8	TGTAATAACGACGGCCAGTGTGCATGTCATCTGTGTGTGT	1437	CAGGAACACGCTATGACCACTATGAAATGTGTAAGGCGA	1558
AE109s9	TGTAATAACGACGGCCAGTTCCTTCAAAATGCGATTTCT	1438	CAGGAACACGCTATGACCTTTCTTCTTGGGCTTT	1559
AE110s1	TGTAATAACGACGGCCAGTCAAGGCATGTCAAGTCTTGAAT	1439	CAGGAACACGCTATGACCTCTCTGCTTGGAAACAGA	1560
AE110s10	TGTAATAACGACGGCCAGTCTGTCTGTGTATCTCCCGA	1440	CAGGAACACGCTATGACCTCTCTGCTTGGAAACAGA	1561
AE110s11	TGTAATAACGACGGCCAGTCAAGACATCTTTTCTCCCG	1441	CAGGAACACGCTATGACCATCCACCAATCTTCCCTC	1562
AE110s12	TGTAATAACGACGGCCAGTGCAGGTCAATGGAAGTGAATTA	1442	CAGGAACACGCTATGACCGACCATTTAGTTTGACC	1563
AE110s2	TGTAATAACGACGGCCAGTGTGATCTGGAGCGACTGTTCTG	1443	CAGGAACACGCTATGACCTTTGCTTGGTGTAGGGA	1564
AE110s3	TGTAATAACGACGGCCAGTCTTTTCAATCATCTATTTGTGG	1444	CAGGAACACGCTATGACCTGACGACTTACTTTTGA	1565
AE110s4	TGTAATAACGACGGCCAGTCAACAGGAACCACTCTGAAG	1445	CAGGAACACGCTATGACCGAGCGCCAGAAATGAGGA	1566
AE110s5	TGTAATAACGACGGCCAGTCTCTTGCATAATTCCTGAATGA	1446	CAGGAACACGCTATGACCAAGGTGTCTCAACCTTA	1567
AE110s6	TGTAATAACGACGGCCAGTCTTGTCTGTACGGGTAAACA	1447	CAGGAACACGCTATGACCTCCCAACAGAGCAGGGAAT	1568
AE110s7	TGTAATAACGACGGCCAGTCAACGGGTACCAATTCATCCC	1448	CAGGAACACGCTATGACCTTAGCAATATATCCAGC	1569
AE110s8	TGTAATAACGACGGCCAGTGAATTTTGGTGTGATAGAGCC	1449	CAGGAACACGCTATGACCTTTTACAAACCACTTT	1570
AE110s9	TGTAATAACGACGGCCAGTGAAGGTGATCCTCTGTAGT	1450	CAGGAACACGCTATGACCTTAAGTGACCTGCCCCAAA	1571

Table XIV
Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A,a ¹	Copies of Rare Allele	Odds Ratio (OR) ²		Upper 95% CL		p(a) ³
									Lower	CL	CL	CL	
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969	0.28	
					0.0251	Exact			3.37	1.2261	10.2718		
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807	0.09	
					0.0062	Exact			5.64	1.2422	34.7611		
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF	0.28	
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF	0.22	
			Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709	0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.